

Abstract

The following invention concerns an enzymatic method for investigating cytosine methylations in DNA sequences. Here, the DNA to be investigated is hybridized to oligonucleotides. The hybrids are reacted with restriction enzymes, which are able to distinguish hemi-methylated DNA double strands either from unmethylated or from homo-methylated DNA double strands. The methylation status of the cytosine positions to be investigated can be determined by different possible detection techniques. The method is particularly suitable for the diagnosis of cancer disorders and other diseases associated with a change of the methylation status as well as for the prognosis of undesired drug effects.